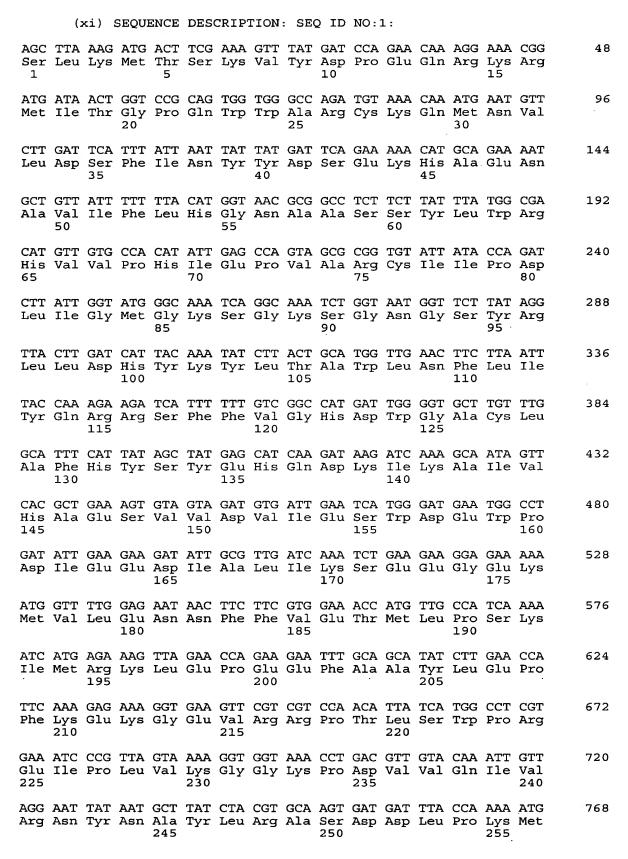
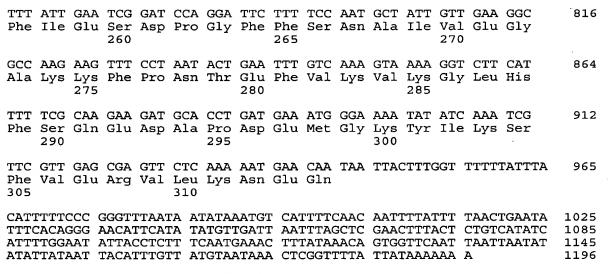
SEQUENCE LISTING

tt,1700

- (1) GENERAL INFORMATION
- (i) APPLICANT: Bryan, Bruce
- (ii) TITLE OF THE INVENTION: BIOLUMINESCENT ARTICLES OF MANUFACTURE
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Brown, Martin, Haller & McClain
 - (B) STREET: 1660 Union Street
 - (C) CITY: San Diego
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 92101-2926
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 11-25-96
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/597,274
 - (B) FILING DATE: 02-06-96
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Seidman, Stephanie L
 - (B) REGISTRATION NUMBER: 33,779
 - (C) REFERENCE/DOCKET NUMBER: 6680-105
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 619-238-0999
 - (B) TELEFAX: 619-238-0062
 - (C) TELEX:
 - (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...942
 - (D) OTHER INFORMATION: Renilla Reinformis Luciferase
- (x) PUBLICATION INFORMATION:

PATENT NO.: 5,418,155





(2) INFORMATION FOR SEQ ID NO:2:

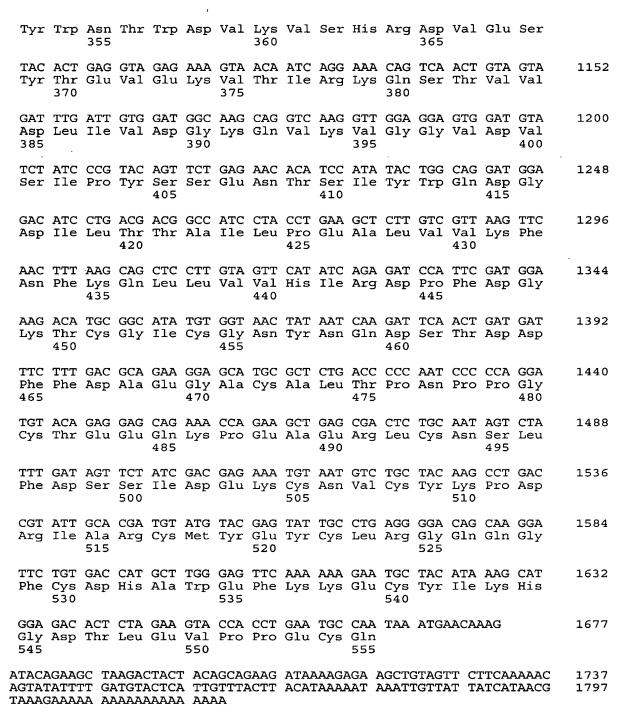
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1821 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...1665
 - (D) OTHER INFORMATION: Cypridina hilgendorfii luciferase
- (x) PUBLICATION INFORMATION:

PATENT NO.: EP 0 387 355 TORAY

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAG Lys								48
TGC Cys	 	 	 	 -	 			96
 ACA Thr	 	 	 		 	 		144
 AGA Arg 50	 	 	 	 	 	 	 	192
AAT Asn								240
TCC Ser								288

			TTT Phe 100													336
			GAC Asp													384
			GCT Ala												GAC Asp	432
			ATT Ile													480
			CCA Pro													528
			GTC Val 180													576
			ATC Ile													624
			ACA Thr													672
			AAT Asn													720
			CCC Pro													768
			TCT Ser 260													816
			TGT Cys													864
			GCT Ala													912
			TAT Tyr													· 960
			TCA Ser													1008
			CAG Gln 340													1056
TAC	TGG	AAC	ACA	TGG	GAT	GTA	AAG	GTT	TCA	CAT	AGA	GAT	GTT	GAG	TCA	1104



(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1643 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

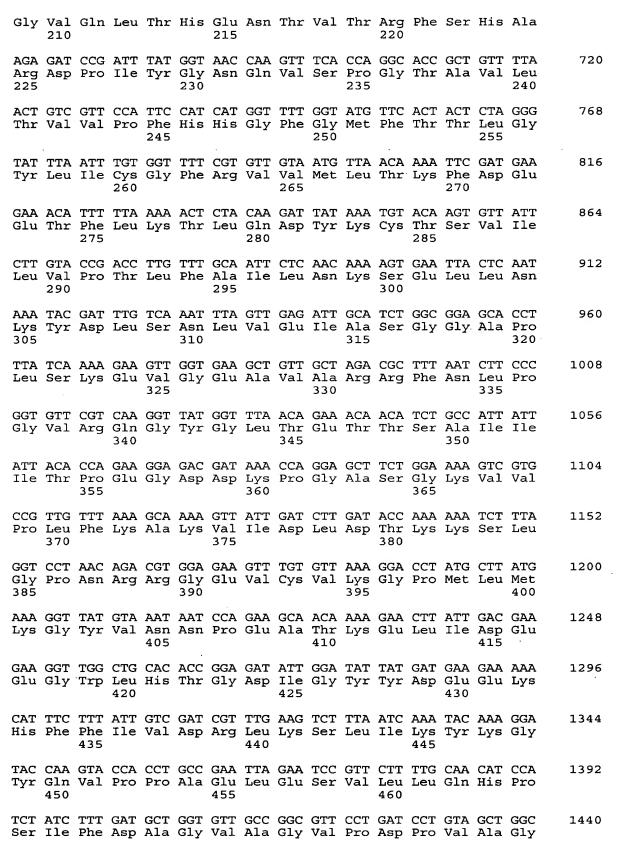
- (A) NAME/KEY: Coding Sequence(B) LOCATION: 1...1644(D) OTHER INFORMATION: Luciola Cruciata Luciferase (Firefly)

(x) PUBLICATION INFORMATION:

PATENT NO.: 4,968,613

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG Met 1													CCT Pro			48
TTT Phe													CGC Arg 30			96
ATG Met																144
ACT Thr																192
CTA Leu 65																240
GCG Ala																288
GGA Gly																336
TTA Leu																384
TTT . Phe																432
GTA Val 145																480
CGA Arg																528
GGT Gly																576
CAA Gln																624
GGC	GTA	CAA	CTT	ACT	CAC	GAA	AAT	ACA	GTC	ACT	AGA	TTT	TCT	CAT	GCT	672



465 470 475 480 GAG CTT CCA GGA GCC GTT GTT GTA CTG GAA AGC GGA AAA AAT ATG ACC Glu Leu Pro GLy Ala Val Val Leu Glu Ser Gly Lys Asn Met Thr 485 490 GAA AAA GAA GTA ATG GAT TAT GTT GCA AGT CAA GTT TCA AAT GCA AAA 1536 Glu Lys Glu Val Met Asp Tyr Val Als Ser Gln Val Ser Asn Ala Lys 505 CGT TTA CGT GGT GGT GTT CGT TTT GTG GAT GAA GTA CCT AAA GGT CTT 1584 Arg Leu Arg Gly Gly Val Arg Phe Val Asp Glu Val Pro Lys Gly Leu 520 ACT GGA AAA ATT GAC GGC AGA GCA ATT AGA GAA ATC CTT AAG AAA CCA 1632 Thr Gly Lys Ile Asp Gly Arg Ala Ile Arg Glu Ile Leu Lys Lys Pro 530 535 GTT GCT AAG ATG 1644 Val Ala Lys Met 545

- (2) INFORMATION FOR SEQ ID NO:4:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1819 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...1664
 - (D) OTHER INFORMATION: Vargula (cypridina) luciferase
- (x) PUBLICATION INFORMATION:
 - JP 3-30678 Osaka (Tsuji)

 - (A) Thompson <u>et al.</u>
 (C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
 - (D) VOLUME: 86
 - (F) PAGES: 1326-1332
 - (G) DATE: (1989)
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

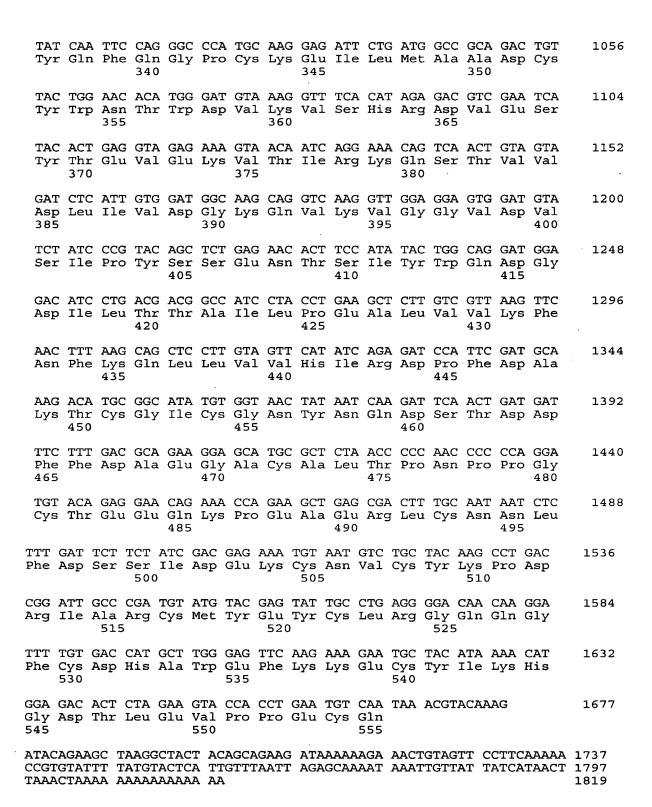
			ATA Ile									48
			GAT Asp 20			 	 		 	 		96
	-	-	CCA	-	_	 -		_	 		_	144

Pro Thr Val Pro Thr Ser Cys Glu Ala Lys Glu Gly Glu Cys Ile Asp

ACC AGA TGC GCA ACA TGT AAA CGA GAT ATA CTA TCA GAT GGA CTG TGT 192 Thr Arg Cys Ala Thr Cys Lys Arg Asp Ile Leu Ser Asp Gly Leu Cys 55 60

GAA AAT AAA CCA GGG AAG ACA TGC TGT AGA ATG TGC CAG TAT GTG ATT 240 Glu Asn Lys Pro Gly Lys Thr Cys Cys Arg Met Cys Gln Tyr Val Ile

65			70			75			80		
				GCT Ala						2	88
				CCT Pro						3	36
				GTA Val						3	84
				ACT Thr 135						4	32
				GCT Ala						4	80
				GCT Ala						5	28
				CCG Pro						5	76
				GAT Asp						6	24
				AAA Lys 215						6	72
				GAT Asp						7	20
				AAC Asn						7	68
				GAA Glu						8:	16
				AAT Asn						8	64
				ATG Met 295						9:	12
				ACA Thr						9	60
				ACT Thr						10	80



(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 958 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence (B) LOCATION: 115...702

 - (D) OTHER INFORMATION: apoaequorin-encoding gene
- (x) PUBLICATION INFORMATION:

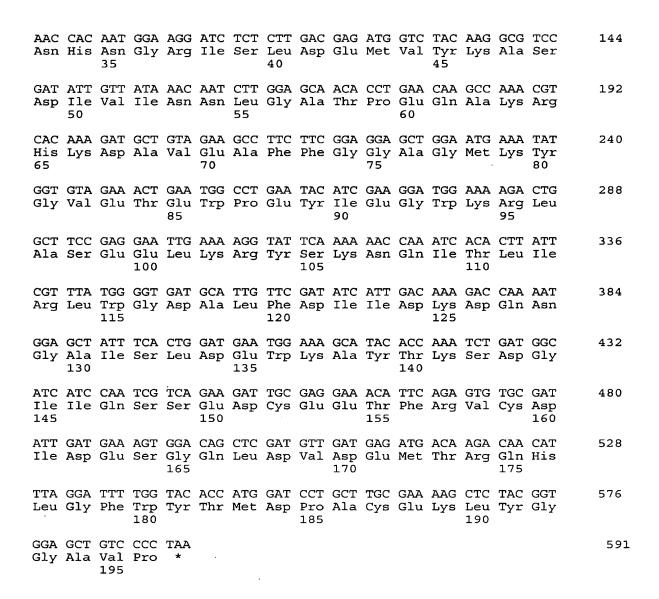
PATENT NO.: 5,093,240

(A) Inouye <u>et al.</u>

- (C) JOURNAL: Proc. Natl. Acad. Sci. U.S.A.
- (D) VOLUME: 82
- (F) PAGES: 3154-3158 (G) DATE: (1985)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGGGG	ecciccc	GGGG	GGGG	GG G(GGGG	3GGG(G GG	GAAT	GCAA	TTC	ATCT:	rtg (CATC	AAAGAA	60
TTACA	ATCAAA	TCTC	TAGT'	IG A	rcaa(CTAA	A TT	GTCT(CGAC	AAC	AACA	AGC i	AAAC	ATG Met 1	117
	AGC AAA Ser Lys														165
	GG ATT														213
His A	AAT GGA Asn Gly 85														261
	TC ATO														309
	SAT GCT Asp Ala														357
	AA ACT														405
	AT GAZ sp Glu 100	ı Leu						-	-				_		453
	GG GG														501

	115					120					125					
														GGT Gly		549
														GAT Asp 160		597
														CAT His		645
														GGT Gly		693
	GTC Val 195		TAAC	GAAG	CTC 1	racg(GTGGT	rg A	ATGC?	CCCI	ra go	BAAGA	ATGA:	r GTC	SATTTTGA	752
TGTT AGA	rgati ACTTA	TTT T	GTAA ATC	ATTA	G AA	ACAGA TAAAA	ATTA VAAA	A ATO	GAA:	CGAT	TAGT	TGT	TTT :	TTTA	CGTTTG ATCAAC AAAAAA	812 872 932 958
		(2)	INI	FORM	MOITA	1 FOR	R SEC	O ID	NO: 6	5:						
	()	(A) (B) (C)	LENC TYPE STRA	NCE (GTH: E: nu ANDEI OLOGY	591 aclei ONESS	base ic ac 3: si	e pai cid ingle	irs								
	i) i) 7) 7)	lii) Lv) <i>F</i> 7) FF 7i) (HYPO ANTIS RAGME	CULE OTHET SENSE ENT T INAL JRE:	CICAI E: NO CYPE:	: NC										
		(B)	LOC	ME/KE CATION HER]	N: 1	L <u>5</u>	588	-	nce ombir	nant	Aequ	orin	n AE(Q1		
	()	c) PU	BLIC	CATIO	N IN	IFORN	ATIC	ON:								
		(B) (C) (D) (F)	TIT IOU IOV IOV PAC		Sequ Enco : Bi : 26 1326	ence ding oche	e Con J Aec emist	npari quori	isons in Is			oleme	entai	cy		
	()	ci) S	SEQUE	ENCE	DESC	RIPT	CION:	SEC	O ID	NO : 6	5:					
														GAC Asp 15		48
														GAT Asp		96



(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 591 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...588
 - (D) OTHER INFORMATION: Recombinant Aequorin AEQ2
- (x) PUBLICATION INFORMATION:



- (A) AUTHORS: Prasher et al.
 (B) TITLE: Sequence Comparisons of Complementary
 DNAs Encoding Aequorin Isotypes
 (C) JOURNAL: Biochemistry
 (D) VOLUME: 26
 (F) PAGES: 1326-1332
 (G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACC Thr									•	48
AGA Arg									!	96
CAC His										44
ATT Ile 50									1:	92
AAA Lys									24	40
GTG Val									2	88
ACT Thr									3:	36
ATA Ile									3	84
GCC Ala 130									4:	32
ATC Ile									41	80
GAT Asp									52	28
GGA Gly					_			_	5'	76
 GCT Ala	_	TAA *							!	591

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 591 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence (B) LOCATION: 1...588

 - (D) OTHER INFORMATION: Recombinant Aequorin AEQ3

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Prasher et al.
- (B) TITLE: Sequence Comparisons of Complementary DNAs Encoding Aequorin Isotypes
- (C) JOURNAL: Biochemistry (D) VOLUME: 26
- (F) PAGES: 1326-1332
- (G) DATE: 1987

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

		TAC Tyr						48
 		CGA Arg						96
 		ATC Ile						144
		AAC Asn						192
 	 	 GGA Gly 70	 	 		 		240
		TGG Trp						288
		GAG Glu						336
 	 	 GCT Ala	 	 _	_			384
		GAT Asp						432

130			135			140			
 ATC Ile	 		 	 	 		 	 	480
 GAT Asp	 		 	 	 		 	 	528
GGA Gly									576
 GCT Ala	 	TAA *							591

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 567 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence (B) LOCATION: 1...567

 - (D) OTHER INFORMATION: Aequorin photoprotein

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: Charbonneau et al.
- (B) TITLE: Amino acid sequence of the calcium-dependent photoprotein aequorin
- (C) JOURNAL: Am. Chem. Soc. (D) VOLUME: 24
- (E) ISSUE: 24
- (F) PAGES: 6762-6771
- (G) DATE: 1985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

	 	ACA Thr	 		 	 	 	 	 48
		TTT Phe 20						 	 96
		ATG Met		-	 		 	 	 144
		CCT Pro							192

	50			55			60			
_		GGA Gly								240
		ATC Ile								288
		AAA Lys	 							336
		ATC Ile 115								384
		GCA Ala	 	 	 	-				432
		GAA Glu								480
		GAT Asp								528
		GCT Ala	 _							567

- (2) INFORMATION FOR SEQ ID NO:10:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs

 - (B) TYPE: nucleic acid(C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 1...588
- (D) OTHER INFORMATION: Aequorin mutant w/increased bioluminescence activitý
 - (x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

- (K) RELEVANT RESIDUES IN SEQ ID NO: 10: Asp 124 changed to Ser
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG ACC AGC GAA CAA TAC TCA GTC AAG CTT ACA CCA GAC TTC GAC AAC Met Thr Ser Glu Gln Tyr Ser Val Lys Leu Thr Pro Asp Phe Asp Asn 48

1		5			10			15		
	TGG Trp									96
	 AAT Asn 35									144
	GTT Val									192
	GAT Asp									240
	GAA Glu									288
	GAG Glu									336
	TGG Trp 115									384
	ATT Ile									432
	 CAA Gln	 	_							480
	 GAA Glu	 								528
	TTT Phe									576
	GTC Val 195									588

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 588 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1...588
 (D) OTHER INFORMATION: Recombinant site-directed Aequorin mutant w/increased biolum. activity

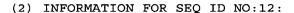
(x) PUBLICATION INFORMATION:

PATENT NO.: 5,360,728

(K) RELEVANT RESIDUES IN SEQ ID NO:11: Glu 135 changed to Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

			TCA Ser							48
			CAC His							96
			TCT Ser						1	44
			CTT Leu 55						1	.92
			GCC Ala						2	40
			CCT Pro						2	88
			AGG Arg						3	36
			TTG Leu						3	84
			TCA Ser 135						4	32
			GAT Asp			Phe			4	80
			CTC Leu						5	28
			ATG Met						5	76
GCT Ala										588



- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 588 base pairs

 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence (B) LOCATION: 1...588

 - (D) OTHER INFORMATION: Recombinant site-directed Aequorin mutant w/increased biolum. activity
- (x) PUBLICATION INFORMATION: PATENT NO.: 5,360,728
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

								TTC Phe		48
								CTT Leu 30		96
-		 	_	-				AAG Lys		144
								GCC Ala		192
								ATG Met		240
								AAA Lys		288.
								ACA Thr 110		336
								GAC Asp		384
								TCT Ser		432
								GTG Val		480





ATT GAT GAA AGT GGA CAG CTC GAT GTT GAT GAG ATG ACA AGA CAA CAT 528 Ile Asp Glu Ser Gly Gln Leu Asp Val Asp Glu Met Thr Arg Gln His 165 170 TTA GGA TTT TGG TAC ACC ATG GAT CCT GCT TGC GAA AAG CTC TAC GGT Leu Gly Phe Trp Tyr Thr Met Asp Pro Ala Cys Glu Lys Leu Tyr Gly 180 185

GGA GCT GTC CCC Gly Ala Val Pro 195

588

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 567 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence (B) LOCATION: 1...567

 - (D) OTHER INFORMATION: Recombinant apoaequorin (AQUALITE®)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAG Lys												48
CAC His												96
GAC Asp											1	L44
 GCA Ala 50	 	 		 				 			1	L92
TTC Phe											2	240
TAC Tyr												288
TCA Ser											3	336
GAT Asp	 										3	884
 AAA Lys 130	 _		_		_	_	-	 -	-	-	4	132





- (2) INFORMATION FOR SEQ ID NO:14:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 236 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (x) PUBLICATION INFORMATION: PATENT NO.: 5,484,723
- (ix) FEATURE:
 - (D) OTHER INFORMATION: Vibrio fisheri Flavin reductase
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Pro Ile Asn Cys Lys Val Lys Ser Ile Glu Pro Leu Ala Cys Asn 1 5 10 15

Thr Phe Arg Ile Leu Leu His Pro Glu Gln Pro Val Ala Phe Lys Ala 20 25 30

Gly Gln Tyr Leu Thr Val Val Met Gly Glu Lys Asp Lys Arg Pro Phe
35 40 45

Ser Ile Ala Ser Ser Pro Cys Arg His Glu Gly Glu Ile Glu Leu His 50 55 60

Ile Gly Ala Ala Glu His Asn Ala Tyr Ala Gly Glu Val Val Glu Ser 65 70 75 80

Met Lys Ser Ala Leu Glu Thr Gly Gly Asp Ile Leu Ile Asp Ala Pro 85 90 95

His Gly Glu Ala Trp Ile Arg Glu Asp Ser Asp Arg Ser Met Leu Leu 100 105 110

Ile Ala Gly Gly Thr Gly Phe Ser Tyr Val Arg Ser Ile Leu Asp His
115 120 125

Cys Ile Ser Gln Gln Ile Gln Lys Pro Ile Tyr Leu Tyr Trp Gly Gly 130 135 140

Arg Asp Glu Cys Gln Leu Tyr Ala Lys Ala Glu Leu Glu Ser Ile Ala 145 150 155 160

Gln Ala His Ser His Ile Thr Phe Val Pro Val Val Glu Lys Ser Glu 165 170 175

Gly Trp Thr Gly Lys Thr Gly Asn Val Leu Glu Ala Val Lys Ala Asp

180 185

190

Phe Asn Ser Leu Ala Asp Met Asp Ile Tyr Ile Ala Gly Arg Phe Glu 195 200

Met Ala Gly Ala Ala Arg Glu Gln Phe Thr Thr Glu Lys Gln Ala Lys 210 215

Lys Glu Gln Leu Phe Gly Asp Ala Phe Ala Phe Ile 230

DOIEGODD COETYDD